MDEADRRLLRRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQRAGSGSRRDQA
RQLIIDLETRGSQAL
PLFISCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLRPEIRKPEVLRPETPR
PVDIGSGGFGDVG
ALESLRGNADLAYILSMEPCGHCLIINNVNFCRESGLRTRTGSNIDCEKLRRRFSSL
HFMVEVKGDLTAK
KMVLALLELARQDHGALDCCVVVILSHGCQASHLQFPGAVYGTDGCPVSVEKIVNI
FNGTSCPSLGGKPK
LFFIQACGGEQKDHGFEVASTSPEDESPGSNPEPDATPFQEGLRTFDQLDAISSLP
TPSDIFVSYSTFPG
FVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFN
FLRKKLFFKTS

FIG. I

1 GCCATGGACG AAGCGGATCG GCGGCTCCTG CGGCGGTGCC GGCTGCGGCT

51 GGTGGAAGAG CTGCAGGTGG ACCAGCTCTG GGACGTCCTG CTGAGCCGCG

101 AGCTGTTCAG GCCCCATATG ATCGAGGACA TCCAGCGGGC AGGCTCTGGA

151 TCTCGGCGGG ATCAGGCCAG GCAGCTGATC ATAGATCTGG AGACTCGAGG

201 GAGTCAGGCT CTTCCTTTGT TCATCTCCTG CTTAGAGGAC ACAGGCCAGG

251 ACATGCTGGC TTCGTTTCTG CGAACTAACA GGCAAGCAGG AAAGTTGTCG

301 AAGCCAACCC TAGAAAACCT TACCCCAGTG GTGCTCAGAC CAGAGATTCG

351 CAAACCAGAG GTTCTCAGAC CGGAAACACC CAGACCAGTG GACATTGGTT

401 CTGGAGGATT CGGTGATGTC GGTGCTCTTG AGAGTTTGAG GGGAAATGCA

451 GATTTGGCTT ACATCCTGAG CATGGAGCCC TGTGGCCACT GCCTCATTAT

501 CAACAATGTG AACTTCTGCC GTGAGTCCGG GCTCCGCACC CGCACTGGCT

551 CCAACATCGA CTGTGAGAAG TTGCGGCGTC GCTTCTCCTC GCTGCATTTC

601 ATGGTGGAGG TGAAGGGCGA CCTGACTGCC AAGAAAATGG TGCTGGCTTT

651 GCTGGAGCTG GCGCGGCAGG ACCACGGTGC TCTGGACTGC TGCGTGGTGG

701 TCATTCTCTC TCACGGCTGT CAGGCCAGCC ACCTGCAGTT CCCAGGGGCT

FIG. 2A

751 GTCTACGGCA CAGATGGATG CCCTGTGTCG GTCGAGAAGA TTGTGAACAT

801 CTTCAATGGG ACCAGCTGCC CCAGCCTGGG AGGGAAGCCC AAGCTCTTTT

851 TCATCCAGGC CTGTGGTGGG GAGCAGAAAG ACCATGGGTT TGAGGTGGCC

901 TCCACTTCCC CTGAAGACGA GTCCCCTGGC AGTAACCCCG AGCCAGATGC

951 CACCCCGTTC CAGGAAGGTT TGAGGACCTT CGACCAGCTG GACGCCATAT

1001 CTAGTTTGCC CACACCCAGT GACATCTTTG TGTCCTACTC TACTTTCCCA

1051 GGTTTTGTTT CCTGGAGGGA CCCCAAGAGT GGCTCCTGGT ACGTTGAGAC

1101 CCTGGACGAC ATCTTTGAGC AGTGGGCTCA CTCTGAAGAC CTGCAGTCCC

1151 TCCTGCTTAG GGTCGCTAAT GCTGTTTCGG TGAAAGGGAT TTATAAACAG

1201 ATGCCTGGTT GCTTTAATTT CCTCCGGAAA AAACTTTTCT TTAAAACATC

1251 ATAAGGCCAG GGCCCCTCAC CCTGCCTTAT CTTGCACCCC AAAGCTTTCC

1301 TGCCCCAGGC CTGAAAGAGG CTGAGGCCTG GACTTTCCTG CAACTCAAGG

1351 ACTTTGNAGC CGGCACAGGG TCTGCTCTTT CTCTGCCAGT GACAGACAGG

1401 CTCTTAGCAG CTTCCAGATT GACGACAAGT GCTGAACAGT GGAGGAAGAG

1451 GGACAGATGA ATGCCGTGGA TTGCACGTGG NCTCTTGAGC AGTGGCTGGT

FIG. 2B

1501 CCAGGGCTAG TGACTTGGTG TCCCATGATC CCTGTGTTGG TCTCTAGGAG

1551 CAGGGATTAA CCTCTGCACT ACTGACAT

FIG. 2C

CTGACTGCCAAGAAAATGGTGCTGGCTTTGCTGGAGCTGG 40
CGCGGCAGGACCACGGTGCTCTGGACTGCTGCGTGGTGGT 80
CATTCTCTCTCACGGCTGTCAGGCCAGCCACCTGCAGTTC 120
CCAGGGGCTGTCTACGGCACAGATGGATGCCCTGTGTCGG 160
TCGAAAAGATTGTGAACATCTTCAATGGGACCAGCTGCCC 200
CAGCCTGGGAGGGAAGCCCAAGCTCTTTTTCATCCAGGCC 240
TGTGGTGGGGAGCAGAAAGACCATGGGTTTGAGGTGGCCT 280
CCACTTCCCCTGAAGACGAGTCCCCTGGCAGTAACCCCGA 320
GCCAGATGCCACCCCGTTCCAGGAAGGTTTGAGGACCTTC 360
GACCAGCTGGACGCCATATCTAGTTTGCCCACACCCAGTG 400
ACATCTTTGTGTCCTACTCTACTTTCCCAGGTTTTGTTTC 440
CTGGAGGGACCCCAAGAGTGGCTCCTGGTACGTTGAGACC 480
CTGGACGACATCTTTGAGCAGTGGGCTCACTCTGAAGACC 520
TGCAGTCCCTCCTGCTTAGGGTCGCTAATGCTGTTTCGGT 560
GAAAGGGATTTATAAACAGATGCCTGGTTGCTTTAATTTC 600
CTCCGGAAAAAACTTTTCTTTTAAAACATCATAAGGCAG 639

FIG. 3

MVLALLELARQDHGALDCCV 20
VVILSHGCQASHLQFPGAVY 40
GTDGCPVSVEKIVNIFNGTS 60
CPSLGGKPKLFFIQACGGEQ 80
KDHGFEVASTSPEDESPGSN 100
PEPDATPFQEGLRTFDQLDA 120
ISSLPTPSDIFVSYSTFPGF 140
VSWRDPKSGSWYVETLDDIF 160
EQWAHSEDLQSLLLRVANAV 180
SVKGIYKQMPGCFNFLRKKL 200
FFM 203

FIG. 4

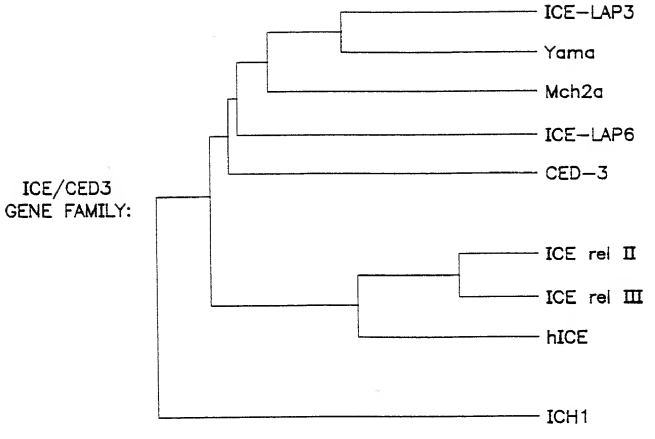
ICE/CED3
GENE FAMILY:
ICE–LAP3
Yama
Mch2a
ICE–LAP6
CED–3
ICE rel II
ICE rel III
hICE
ICH1

FIG. 5

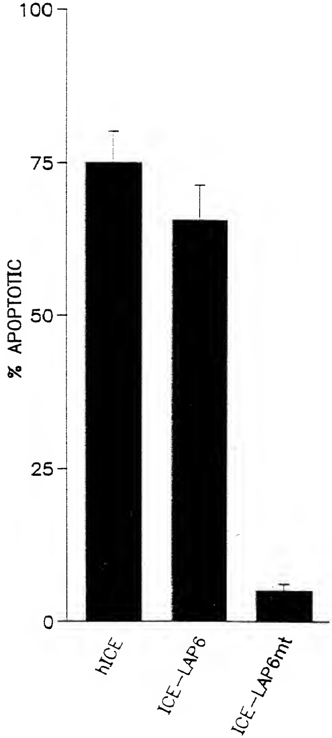

FIG. 6